



## SEQUENCE LISTING

<110> Bruck, Claudine  
Godart, Stephane Andre Georges  
Marc-Hand, Martine

<120> FUSION PROTEINS COMPRISING HIV-1 TAT  
AND/OR NEF PROTEINS

<130> B45110C1

<140> 10/687,060

<141> 2003-10-16

<150> 09/509,239

<151> 2000-03-23

<150> PCT/EP98/06040

<151> 1998-09-17

<150> GB 9720585.0

<151> 1997-09-26

<160> 27

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 1

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23

<210> 2

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 2

cggtactag tgcagttctt gaa

23

<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 3

atcggtactag tgagccagta gatc

24

<210> 4  
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<220>  
<223> PCR primer

<400> 4  
cggtactag tttccttcgg gcct

24

<210> 5  
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<400> 5  
atcgtccatg gagccagtag atc

23

<210> 6  
<211> 441  
<212> DNA  
<213> Haemophilus influenzae

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agccattcat caaatatggc gaatacccaa atgaaatcag acaaaatcat tattgctcac 120  
cgtggtgcta gcggttattt accagagcat acgtagaat ctaaagcact tgcttttgca 180  
caacaggctg attattttaga gcaagattta gcaatgacta aggatggtcg tttagtgggt 240  
attcacgatc acttttttaga tggcttgact gatgttgca aaaaattccc acatcgatc 300  
cgtaaagatg gccgttacta tgatcatgac tttaccttaa aagaaattca aagtttagaa 360  
atgacagaaa actttgaaac catggccacg tgtgatcaga gctcaactag tggccaccat 420  
caccatcacc attaacttag a 441

<210> 7  
<211> 144  
<212> PRT  
<213> Haemophilus influenzae

<400> 7  
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Ala Gly Cys Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys  
20 25 30  
Ser Asp Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro  
35 40 45  
Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp  
50 55 60  
Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val  
65 70 75 80  
Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe  
85 90 95  
Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr  
100 105 110  
Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met  
115 120 125  
Ala Thr Cys Asp Gln Ser Ser Thr Ser Gly His His His His His

<210> 8  
 <211> 648  
 <212> DNA  
 <213> Human Immunodeficiency Virus

<400> 8  
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 agacgagctg agccagcagc agatgggggtg ggagcagcat ctcgagacct ggaaaaacat 120  
 ggagcaatca caagtagcaa tacagcagct accaatgctg cttgtgcctg gctagaagca 180  
 caagaggagg aggaggtggg ttttccagtc acacctcagg tacctttaag accaatgact 240  
 tacaaggcag ctgtagatct tagccacttt ttaaaagaaa aggggggact ggaagggcta 300  
 attcactccc aacgaagaca agatatacctt gatctgtgga tctaccacac acaaggctac 360  
 ttccctgatt ggcagaacta cacaccaggg ccaggggtca gatatccact gaccttttga 420  
 tggtgctaca agctagtacc agttgagcca gataaggtag aagaggccaa taaaggagag 480  
 aacaccagct tgttacaccc tgtgagcctg catggaatgg atgaccctga gagagaagtg 540  
 ttagagtggg ggtttgacag ccgcctagca tttcatcacg tggcccgaga gctgcatccg 600  
 gagtacttca agaactgcac tagtggccac catcaccatc accattaa 648

<210> 9  
 <211> 215  
 <212> PRT  
 <213> Human Immunodeficiency Virus

<400> 9  
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 20 25 30  
 Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr  
 35 40 45  
 Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu  
 50 55 60  
 Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr  
 65 70 75 80  
 Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly  
 85 90 95  
 Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu  
 100 105 110  
 Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr  
 115 120 125  
 Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys  
 130 135 140  
 Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu  
 145 150 155 160  
 Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro  
 165 170 175  
 Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His  
 180 185 190  
 His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser  
 195 200 205  
 Gly His His His His His His  
 210 215

<210> 10  
 <211> 288  
 <212> DNA  
 <213> Human Immunodeficiency Virus

<400> 10  
atggagccag tagatcctag actagagccc tggaagcatc caggaagtca gcctaaaact 60  
gcttgtacca attgctattg taaaaagtgt tgcttttcatt gccaaagtttg tttcataaca 120  
aaagccttag gcatctccta tggcaggaag aagcggagac agcgacgaag acctcctcaa 180  
ggcagtcaga ctcacaaagt ttctctatca aagcaaccca cctcccaatc ccgagggggac 240  
ccgacaggcc cgaaggaaac tagtggccac catcaccatc accattaa 288

<210> 11

<211> 95

<212> PRT

<213> Human Immunodeficiency Virus

<400> 11

Met	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser
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Gln	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe
			20					25					30		
His	Cys	Gln	Val	Cys	Phe	Ile	Thr	Lys	Ala	Leu	Gly	Ile	Ser	Tyr	Gly
		35					40					45			
Arg	Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln	Thr
		50				55					60				
His	Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Arg	Gly	Asp
65					70					75					80
Pro	Thr	Gly	Pro	Lys	Glu	Thr	Ser	Gly	His	His	His	His	His	His	
				85					90					95	

<210> 12

<211> 909

<212> DNA

<213> Human Immunodeficiency Virus

<400> 12

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ggagcaatca	caagtagcaa	tacagcagct	accaatgctg	cttgtgcctg	gctagaagca	180
caagaggagg	aggaggtggg	ttttccagtc	acacctcagg	tacctttaag	accaatgact	240
tacaaggcag	ctgtagatct	tagccacttt	ttaaaagaaa	aggggggact	ggaaggggcta	300
attcactccc	aacgaagaca	agatatacctt	gatctgtgga	tctaccacac	acaaggctac	360
ttccctgatt	ggcagaacta	cacaccaggg	ccaggggtca	gatataccact	gacctttgga	420
tggtgctaca	agctagtacc	agttgagcca	gataaggtag	aagaggccaa	taaaggagag	480
aacaccagct	tgttacaccc	tgtgagcctg	catggaatgg	atgaccctga	gagagaagtg	540
ttagagtggg	ggtttgacag	ccgcctagca	tttcatcacg	tggcccgaga	gctgcatccg	600
gagtacttca	agaactgcac	tagtgagcca	gtagatccta	gactagagcc	ctggaagcat	660
ccaggaagtc	agcctaaaac	tgcttgtacc	aattgctatt	gtaaaaagtg	ttgctttcat	720
tgccaagttt	gtttcataac	aaaagcctta	ggcatctcct	atggcaggaa	gaagcggaga	780
cagcgacgaa	gacctcctca	aggcagtcag	actcatcaag	tttctctatc	aaagcaaccc	840
acctcccaat	cccaggggga	cccagcaggc	ccgaaggaaa	ctagtggcca	ccatcaccat	900
caccattaa						909

<210> 13

<211> 302

<212> PRT

<213> Human Immunodeficiency Virus

<400> 13

Met	Gly	Gly	Lys	Trp	Ser	Lys	Ser	Ser	Val	Val	Gly	Trp	Pro	Thr	Val
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Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala	Ala	Asp	Gly	Val	Gly	Ala
			20					25					30		

Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	Ser	Asn	Thr
	35						40					45			
Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	Glu	Glu	Glu
	50					55					60				
Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met	Thr
	65				70					75					80
Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly	Gly
			85						90					95	
Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp	Leu
			100					105					110		
Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
	115						120					125			
Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	Lys
	130					135					140				
Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly	Glu
	145				150					155					160
Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro
			165					170						175	
Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe	His
			180					185					190		
His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	Thr	Ser
	195						200					205			
Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser	Gln
	210					215					220				
Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe	His
	225				230					235					240
Cys	Gln	Val	Cys	Phe	Ile	Thr	Lys	Ala	Leu	Gly	Ile	Ser	Tyr	Gly	Arg
			245						250					255	
Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln	Thr	His
			260					265					270		
Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Arg	Gly	Asp	Pro
	275						280					285			
Thr	Gly	Pro	Lys	Glu	Thr	Ser	Gly	His	His	His	His	His	His		
	290					295					300				

<210> 14  
 <211> 1029  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fusion construct

<400> 14  
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cggtgtgcta gcggttattt accagagcat acgttagaat ctaaagcact tgcttttgca 180  
 caacaggctg attatttaga gcaagattta gcaatgacta aggatggctg tttagtgggt 240  
 attcacgac acttttttaga tggcttgact gatgttgca aaaaattccc acatcgatcat 300  
 cgtaaagatg gccgttacta tgtcatcgac tttacccttaa aagaaattca aagtttagaa 360  
 atgacagaaa actttgaaac catgggtggc aagtgggtcaa aaagtagtgt ggttggatgg 420  
 cctactgtaa gggaaagaat gagacgagct gagccagcag cagatggggg gggagcagca 480  
 tctcgagacc tggaaaaaca tggagcaatc acaagtagca atacagcagc taccaatgct 540  
 gcttgtgcct ggctagaagc acaagaggag gaggaggtgg gttttccagt cacacctcag 600  
 gtacctttaa gaccaatgac ttacaaggca gctgtagatc ttagccactt tttaaaagaa 660  
 aaggggggac tgggaagggt aattcactcc caacgaagac aagatatacct tgatctgtgg 720  
 atctaccaca cacaaggcta cttccctgat tggcagaact acacaccagg gccaggggtc 780  
 agatatccac tgacctttgg atggtgctac aagctagtag cagttgagcc agataaggta 840  
 gaagaggcca ataaaggaga gaacaccagc ttgttacacc ctgtgagcct gcatggaatg 900

gatgaccctg agagagaagt gttagagtgg aggtttgaca gccgcctagc atttcatcac 960  
 gtggcccgag agctgcatcc ggagtacttc aagaactgca ctagtggcca ccatcaccat 1020  
 caccattaa 1029

<210> 15  
 <211> 324  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fusion construct

<400> 15  
 Cys Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys Ser Asp  
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 Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro Glu His  
 20 25 30  
 Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp Tyr Leu  
 35 40 45  
 Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val Ile His  
 50 55 60  
 Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe Pro His  
 65 70 75 80  
 Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr Leu Lys  
 85 90 95  
 Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met Gly Gly  
 100 105 110  
 Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val Arg Glu Arg  
 115 120 125  
 Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala Ala Ser Arg  
 130 135 140  
 Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr Ala Ala Thr  
 145 150 155 160  
 Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu Glu Val Gly  
 165 170 175  
 Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala  
 180 185 190  
 Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly  
 195 200 205  
 Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr  
 210 215 220  
 His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro  
 225 230 235 240  
 Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro  
 245 250 255  
 Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser  
 260 265 270  
 Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu  
 275 280 285  
 Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His His Val Ala  
 290 295 300  
 Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser Gly His His  
 305 310 315 320  
 His His His His

<210> 16  
 <211> 1290  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Fusion construct

<400> 16

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cgtggtgcta gcggttattt accagagcat acgttagaat ctaaagcact tgcgtttgca 180
caacaggctg attattttaga gcaagattta gcaatgacta aggatggtcg tttagtgggt 240
attcacgatac acttttttaga tggcttgact gatgttgca aaaaattccc acatcgtcac 300
cgtaaagatg gccgttacta tgtcatcgac tttaccttaa aagaaattca aagtttagaa 360
atgacagaaa actttgaaac catgggtggc aagtgggtcaa aaagtagtgt gggtggatgg 420
cctactgtaa gggaaagaat gagacgagct gagccagcag cagatggggg gggagcagca 480
tctcgagacc tggaaaaaca tggagcaatc acaagtagca atacagcagc taccaatgct 540
gcttgtgcct ggctagaagc acaagaggag gaggaggtgg gttttccagt cacacctcag 600
gtacctttta gaccaatgac ttacaaggca gctgtagatc ttagccactt tttaaaagaa 660
aaggggggac tggaagggtc aattcactcc caacgaagac aagatatacct tgatctgtgg 720
atctaccaca cacaaggcta cttccctgat tggcagaact acacaccagg gccaggggtc 780
agatatccac tgacctttgg atggtgctac aagctagtag cagttgagcc agataaggta 840
gaagaggcca ataaaggaga gaacaccagc ttgttacacc ctgtgagcct gcatggaatg 900
gatgaccctg agagagaagt gttagagtgg aggtttgaca gccgcctagc atttcatcac 960
gtggccccgag agctgcatcc ggagtacttc aagaactgca ctagttagcc agtagatcct 1020
agactagagc cctggaagca tccaggaagt cagcctaaaa ctgcttgtag caattgctat 1080
tgtaaaaagt gttgctttca ttgccaagtt tgtttcataa caaaagcctt aggcattctc 1140
tatggcagga agaagcggag acagcgacga agacctcctc aaggcagtca gactcatcaa 1200
gtttctctat caaagcaacc cacctcccaa tcccgagggg acccgacagg cccgaaggaa 1260
actagtggcc accatcacca tcaccattaa 1290
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<210> 17

<211> 411

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion construct

<400> 17

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Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro Glu His
 20          25          30
Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp Tyr Leu
 35          40          45
Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val Ile His
 50          55          60
Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe Pro His
 65          70          75          80
Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr Leu Lys
 85          90          95
Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met Gly Gly
100          105          110
Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val Arg Glu Arg
115          120          125
Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala Ala Ser Arg
130          135          140
Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr Ala Ala Thr
145          150          155          160
Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu Glu Val Gly
165          170          175
Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala
180          185          190
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Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly	Gly	Leu	Glu	Gly
	195						200					205			
Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp	Leu	Trp	Ile	Tyr
	210					215					220				
His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	Pro	Gly	Pro
225					230					235					240
Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	Lys	Leu	Val	Pro
				245					250					255	
Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly	Glu	Asn	Thr	Ser
			260					265					270		
Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro	Glu	Arg	Glu
		275					280					285			
Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe	His	His	Val	Ala
	290					295					300				
Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	Thr	Ser	Glu	Pro	Val
305					310					315					320
Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser	Gln	Pro	Lys	Thr
				325					330					335	
Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe	His	Cys	Gln	Val
			340					345					350		
Cys	Phe	Ile	Thr	Lys	Ala	Leu	Gly	Ile	Ser	Tyr	Gly	Arg	Lys	Lys	Arg
	355						360					365			
Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln	Thr	His	Gln	Val	Ser
	370					375					380				
Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Arg	Gly	Asp	Pro	Thr	Gly	Pro
385					390					395					400
Lys	Glu	Thr	Ser	Gly	His	His	His	His	His	His					
			405					410							

<210> 18  
 <211> 981  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fusion construct

<400> 18  
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 cttgcgtttg cacaacaggc tgattatttta gagcaagatt tagcaatgac taaggatggg 180  
 cgtttagtggt ttattcacga tcactttttta gatggccttga ctgatgttgc gaaaaaattc 240  
 ccacatcgtc atcgtaaaga tggccgttac tatgtcatcg actttacctt aaaagaaatt 300  
 caaagttagg aaatgacaga aaactttgaa accatgggtg gcaagtggtc aaaaagtagt 360  
 gtgggttgat ggcctactgt aagggaagaa atgagacgag ctgagccagc agcagatggg 420  
 gtgggagcag catctcgaga cctggaaaaa catggagcaa tcacaagtag caatacagca 480  
 gctaccaatg ctgcttgtgc ctggctagaa gcacaagagg aggaggagggt gggttttcca 540  
 gtcacacctc aggtaccttt aagaccaatg acttacaagg cagctgtaga tcttagccac 600  
 tttttaaaag aaaagggggg actggaaggg ctaattcact cccaacgaag acaagatatc 660  
 cttgatctgt ggatctacca cacacaaggc tacttccttg attggcagaa ctacacacca 720  
 gggccagggg tcagatatcc actgaccttt ggatgggtgct acaagctagt accagttgag 780  
 ccagataagg tagaagaggc caataaagga gagaacacca gcttggttaca ccctgtgagc 840  
 ctgcatggaa tggatgacct tgagagagaa gtgttagagt ggaggtttga cagccgccta 900  
 gcatttcac acgtggccc agagctgcat ccggagtact tcaagaactg cactagtggc 960  
 caccatcacc atcaccatta a 981

<210> 19  
 <211> 326  
 <212> PRT  
 <213> Artificial Sequence



<220>

<223> Fusion construct

<400> 19

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Met Asp Pro Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys
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Ser Asp Lys Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
 20          25          30
Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp
 35          40          45
Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
 50          55          60
Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
 65          70          75          80
Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
 85          90          95
Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
100          105          110
Gly Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val Arg
115          120          125
Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala Ala
130          135          140
Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr Ala
145          150          155          160
Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu Glu
165          170          175
Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr
180          185          190
Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu
195          200          205
Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp
210          215          220
Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro
225          230          235          240
Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu
245          250          255
Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn
260          265          270
Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu
275          280          285
Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His His
290          295          300
Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser Gly
305          310          315          320
His His His His His
325
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<210> 20

<211> 1242

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion construct

<400> 20

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attattgctc accgtggtgc tagcggttat ttaccagagc atacgttaga atctaaagca 120
cttgcgtttg cacaacaggc tgattattta gagcaagatt tagcaatgac taaggatggt 180
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cgtttagtgg ttattcacga tcacttttta gatggcttga ctgatgttgc gaaaaaattc 240
ccacatcgtc atcgtaaaga tggccgttac tatgtcatcg actttacctt aaaagaaatt 300
caaagttagt aaatgacaga aaactttgaa accatgggtg gcaagtggtc aaaaagtagt 360
gtggttggat ggcctactgt aagggaaaga atgagacgag ctgagccagc agcagatggg 420
gtgggagcag catctcgaga cctggaaaaa catggagcaa tcacaagtag caatacagca 480
gctaccaatg ctgcttgtgc ctggctagaa gcacaagagg aggaggaggt gggttttcca 540
gtcacacctc aggtaccttt aagaccaatg acttacaagg cagctgtaga tcttagccac 600
tttttaaaag aaaagggggg actggaaggg ctaattcact cccaacgaag acaagatatc 660
cttgatctgt ggatctacca cacacaaggc tacttccctg attggcagaa ctacacacca 720
gggccagggg tcagatatcc actgaccttt ggatgggtgt acaagctagt accagttgag 780
ccagataagg tagaagaggc caataaagga gagaacacca gcttgttaca ccctgtgagc 840
ctgcatggaa tggatgacct tgagagagaa gtgttagagt ggaggtttga cagccgccta 900
gcatttcatc acgtggcccg agagctgcat ccggagtact tcaagaactg cactagttag 960
ccagtagatc ctagactaga gccctggaag catccaggaa gtcagcctaa aactgcttgt 1020
accaattgct attgtaaaaa gtgttgcttt cattgccaag tttgtttcat aacaaaagcc 1080
ttaggcatct cctatggcag gaagaagcgg agacagcgac gaagacctcc tcaaggcagt 1140
cagactcatc aagtttctct atcaaagcaa cccacctccc aatcccaggg ggacccgaca 1200
ggcccgaagg aaactagtgg ccaccatcac catcaccatt aa 1242

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<210> 21

<211> 413

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion construct

<400> 21

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Met Asp Pro Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys
 1          5          10          15
Ser Asp Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
 20          25          30
Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp
 35          40          45
Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
 50          55          60
Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
 65          70          75          80
Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
 85          90          95
Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
100          105          110
Gly Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val Arg
115          120          125
Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala Ala
130          135          140
Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr Ala
145          150          155          160
Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu Glu
165          170          175
Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr
180          185          190
Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu
195          200          205
Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp
210          215          220
Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro
225          230          235          240
Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu
245          250          255

```

Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly	Glu	Asn
			260					265					270		
Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro	Glu
		275					280					285			
Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe	His	His
		290				295					300				
Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	Thr	Ser	Glu
305					310					315					320
Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser	Gln	Pro
				325					330					335	
Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe	His	Cys
			340					345					350		
Gln	Val	Cys	Phe	Ile	Thr	Lys	Ala	Leu	Gly	Ile	Ser	Tyr	Gly	Arg	Lys
		355					360					365			
Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln	Thr	His	Gln
	370				375						380				
Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Arg	Gly	Asp	Pro	Thr
385					390					395					400
Gly	Pro	Lys	Glu	Thr	Ser	Gly	His	His	His	His	His	His			

405

410

<210> 22  
 <211> 288  
 <212> DNA  
 <213> Human Immunodeficiency Virus

<400> 22  
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 gcttgtagca attgctattg taaaaagtgt tgctttcatt gccagtttg tttcataaca 120  
 gctgccttag gcatctccta tggcaggaag aagcggagac agcgacgaag acctcctcaa 180  
 ggcagtcaga ctcatcaagt ttctctatca aagcaacca cctcccaatc caaaggggag 240  
 ccgacaggcc cgaaggaaac tagtggccac catcaccatc accattaa 288

<210> 23  
 <211> 95  
 <212> PRT  
 <213> Human Immunodeficiency Virus

Met	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser
1				5					10					15	
Gln	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe
			20					25					30		
His	Cys	Gln	Val	Cys	Phe	Ile	Thr	Ala	Ala	Leu	Gly	Ile	Ser	Tyr	Gly
		35					40					45			
Arg	Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln	Thr
	50					55					60				
His	Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Lys	Gly	Glu
65						70				75					80
Pro	Thr	Gly	Pro	Lys	Glu	Thr	Ser	Gly	His	His	His	His	His	His	
				85					90					95	

<210> 24  
 <211> 909  
 <212> DNA  
 <213> Human Immunodeficiency Virus

<400> 24

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atgggtggca agtgggtcaaa aagtagtggtg gttgggatggc ctactgtaag ggaaagaatg 60
agacgagctg agccagcagc agatgggggtg ggagcagcat ctcgagacct ggaaaaacat 120
ggagcaatca caagtagcaa tacagcagct accaatgctg cttgtgcctg gctagaagca 180
caagaggagg aggaggtggg ttttccagtc acacctcagg tacctttaag accaatgact 240
tacaaggcag ctgtagatct tagccacttt ttaaaagaaa aggggggact ggaagggcta 300
attcactccc aacgaagaca agatatacctt gatctgtgga tctaccacac acaagggtac 360
ttccctgatt ggcagaacta cacaccaggg ccaggggtca gatatccact gacctttgga 420
tggtgctaca agctagtacc agttgagcca gataaggtag aagaggccaa taaaggagag 480
aacaccagct tgttacaccc tgtgagcctg catggaatgg atgaccctga gagagaagtg 540
ttagagtggg ggtttgacag ccgcctagca tttcatcacg tggcccgaaga gctgcatccg 600
gagtacttca agaactgcac tagtgagcca gtagatccta gactagagcc ctggaagcat 660
ccaggaagtc agcctaaaac tgcttgtagc aattgctatt gtaaaaagtg ttgctttcat 720
tgccaagttt gtttcataac agctgcctta ggcattctct atggcaggaa gaagcggaga 780
cagcgacgaa gacctcctca aggcagtcag actcatcaag tttctctatc aaagcaaccc 840
acctcccaat ccaaagggga gccgacaggc ccgaaggaaa ctagtggcca ccatcaccat 900
caccattaa                                     909

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<210> 25

<211> 302

<212> PRT

<213> Human Immunodeficiency Virus

<400> 25

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Met Gly Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val
 1          5          10          15
Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala
 20          25          30
Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr
 35          40          45
Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu
 50          55          60
Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
 65          70          75          80
Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
 85          90          95
Leu Glu Gly Leu Ile His Ser Gln Arg Gln Asp Ile Leu Asp Leu
100          105          110
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
115          120          125
Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
130          135          140
Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu
145          150          155          160
Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro
165          170          175
Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
180          185          190
His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
195          200          205
Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
210          215          220
Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
225          230          235          240
Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg
245          250          255
Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His
260          265          270
Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro
275          280          285
Thr Gly Pro Lys Glu Thr Ser Gly His His His His His His
290          295          300

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<210> 26  
<211> 57  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> MCS polylinker

<400> 26  
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<210> 27  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> MCS polylinker

<400> 27  
Thr Ser Gly His His His His His His  
1 5